



## ORIGINAL ARTICLE

# Genomic analysis of Bornean geckos (Gekkonidae: *Cyrtodactylus*) reveals need for updated taxonomy

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## Abstract

Using molecular genetic data, recognised diversity within the gecko genus *Cyrtodactylus* has more than doubled, with many lineages that were once thought to be wide-ranging being delimited into multiple independent species. On the Southeast Asian island of Borneo, there has been a recent renewed focus on reptile taxonomy, as genetic data have demonstrated a high amount of unrecognised biodiversity. We herein advance this taxonomic trend by delimiting three distinct species within the *Cyrtodactylus consobrinus* species complex: *C. consobrinus*, *C. kapitensis* sp. n., and *C. hutan* sp. n. To do so, we use a combination of ddRAD-seq and single-locus data, and morphological data. Using genomic data, we test species and population boundaries within the *consobrinus* species complex and show minimal population structure but high species-level diversity. Despite not finding uniquely diagnostic morphological characters to delimit the new species, we suggest a combination of characters that can be used to identify each lineage. Lastly, we use our data to comment on the status of *C. malayanus*, with indications that this lineage is also better considered a species complex. These data highlight the prevalence of unrecognised lineages on Borneo, many of which face threats due to increasing deforestation and other anthropogenic pressures.

## KEYWORDS

ddRADseq, morphology, multispecies coalescent, population genetics, Southeast Asia, species delimitation